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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=3; day=10; hr=10; min=20; sec=26; ms=768; ]

=====

\*\*\*\*\*

Reviewer Comments:

<210> 696  
<211> 160  
<212> PRT  
<213> Homo sapiens  
<220>  
<221> MOD\_RES  
<222> (95)  
<223> Variable amino acid  
<220>  
<221> MOD\_RES  
<222> (105)  
<223> Variable amino acid  
<220>  
<221> MOD\_RES  
<222> (118)  
<223> Variable amino acid  
<220>  
<221> MOD\_RES  
<222> (120)  
<223> Variable amino acid  
<400> 696

Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Ser	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly
1					5				10					15	
Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met
					20				25					30	
Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln
								35				40		45	
Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val
								50			55		60		

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr				
65	70	75		80
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Xaa				
	85	90		95
Gly Lys Glu Tyr Lys Cys Lys Val Ser Xaa Lys Gly Leu Pro Ser Ser				
	100	105		110
Ile Glu Lys Thr Ile Ser Xaa Ala Xaa Gly Gln Pro Arg Glu Pro Gln				
	115	120		125
Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val				
	130	135		140
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val				
	145	150		155
				160

A mandatory feature is required to cover every "Xaa" used in a sequence. SEQ ID # 696 does not have a feature to cover the "Xaa" at positions 96, 106, 119 and 121. Please make all necessary changes.

\*\*\*\*\*

Application No: 10627556 Version No: 2.0

**Input Set:**

**Output Set:**

**Started:** 2009-02-18 18:53:57.456  
**Finished:** 2009-02-18 18:54:16.952  
**Elapsed:** 0 hr(s) 0 min(s) 19 sec(s) 496 ms  
**Total Warnings:** 631  
**Total Errors:** 13  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41)
W 213	Artificial or Unknown found in <213> in SEQ ID (42)
W 213	Artificial or Unknown found in <213> in SEQ ID (43)
W 213	Artificial or Unknown found in <213> in SEQ ID (44)

**Input Set:**

**Output Set:**

**Started:** 2009-02-18 18:53:57.456  
**Finished:** 2009-02-18 18:54:16.952  
**Elapsed:** 0 hr(s) 0 min(s) 19 sec(s) 496 ms  
**Total Warnings:** 631  
**Total Errors:** 13  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (201)
W 402	Undefined organism found in <213> in SEQ ID (202)
W 402	Undefined organism found in <213> in SEQ ID (203)
W 402	Undefined organism found in <213> in SEQ ID (204)
W 402	Undefined organism found in <213> in SEQ ID (205)
W 402	Undefined organism found in <213> in SEQ ID (206)
E 257	Invalid sequence data feature in <221> in SEQ ID (212)
E 257	Invalid sequence data feature in <221> in SEQ ID (216)
W 402	Undefined organism found in <213> in SEQ ID (451)
W 402	Undefined organism found in <213> in SEQ ID (452)
W 402	Undefined organism found in <213> in SEQ ID (457)
W 402	Undefined organism found in <213> in SEQ ID (458)
W 251	Found intentionally skipped sequence in SEQID (520 )
W 251	Found intentionally skipped sequence in SEQID (521 )
W 251	Found intentionally skipped sequence in SEQID (522 )
W 251	Found intentionally skipped sequence in SEQID (523 )
W 251	Found intentionally skipped sequence in SEQID (524 )
W 251	Found intentionally skipped sequence in SEQID (525 )
W 251	Found intentionally skipped sequence in SEQID (526 )
W 251	Found intentionally skipped sequence in SEQID (527 )
W 251	Found intentionally skipped sequence in SEQID (639 )

**Input Set:**

**Output Set:**

**Started:** 2009-02-18 18:53:57.456  
**Finished:** 2009-02-18 18:54:16.952  
**Elapsed:** 0 hr(s) 0 min(s) 19 sec(s) 496 ms  
**Total Warnings:** 631  
**Total Errors:** 13  
**No. of SeqIDs Defined:** 699  
**Actual SeqID Count:** 699

Error code	Error Description
W 251	Found intentionally skipped sequence in SEQID (640 )
W 251	Found intentionally skipped sequence in SEQID (643 )
W 251	Found intentionally skipped sequence in SEQID (646 )
W 251	Found intentionally skipped sequence in SEQID (680 )
W 251	Found intentionally skipped sequence in SEQID (681 )
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
E 257	Invalid sequence data feature in <221> in SEQ ID (685)
W 251	Found intentionally skipped sequence in SEQID (688 )
W 251	Found intentionally skipped sequence in SEQID (689 )
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 257	Invalid sequence data feature in <221> in SEQ ID (696)
E 341	'Xaa' position not defined SEQID (696) POS (96)
E 341	'Xaa' position not defined SEQID (696) POS (106)
E 341	'Xaa' position not defined SEQID (696) POS (119)
E 341	'Xaa' position not defined SEQID (696) POS (121)
W 251	Found intentionally skipped sequence in SEQID (699 )

<110> Ledbetter, Jeffrey A.  
Hayden-Ledbetter, Martha  
Thompson, Peter A.

## <120> BINDING CONSTRUCTS AND METHODS FOR USE THEREOF

<130> 910180.401C2

<140> 10627556

<141> 2003-07-26

<150> US 10/053,530

<151> 2002-01-17

<150> US 60/367,358

<151> 2001-01-17

<160> 699

<170> PatentIn version 3.2

<210> 1

<211> 714

<212> DNA

<213> *Homo sapiens*

<400> 1

tctgtacagg agcccaaata ttgtacaaa actcacat gcccaccgtg cccagcacct 60  
gaactcctgg ggggaccgtc agtcttcctc ttcccccaa aacccaagga caccctcatg 120  
atctcccgga cccctgaggt cacatgcgtg gtgggtggacg tgagccacga agaccctgag 180  
gtcaagtca actggtaacgt ggacggcgtg gaggtgcata atgccaagac aaagccgcgg 240  
gaggagcagt acaacacgcac gtaccgtgtg gtcaagcgtcc tcaccgtcct gcaccaggac 300  
tggctgaatg gcaaggagta caagtgcacag gtctccaaca aagccctccc agccccatc 360  
gagaaaacaa tctccaaagc caaagggcag ccccgagaac cacaggtgt a caccctgccc 420  
ccatcccggt atgagctgac caagaaccag gtcaagcctga cctgcctggt caaaggcttc 480  
tatcccgacgc acatcgccgt ggagtgggag agcaatggc agccggagaa caactacaag 540  
accacgcctc ccgtgtcgtt cccgacggc tccttcttcc tctacagcaa gtcaccgtg 600  
gacaagagca ggtggcagca ggggaacgtc ttctcatgtc ccgtgtatgc tgaggcttg 660  
cacaaccact acacgcagaa gagcctctcc ctgtctccgg gttaatgatc taga 714

<210> 2

<211> 235

<212> PRT

<213> *Homo sapiens*

<400> 2

Ser	Asp	Gln	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro		
1															15		
Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro		
														20	25	30	
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr		
														35	40	45	
Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn		
														50	55	60	
Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg		
														65	70	75	80
Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val		
														85	90	95	

Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser
100							105					110			
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys
115							120					125			
Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp
130				135						140					
Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe
145						150				155			160		
Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu
	165						170				175				
Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe
	180						185				190				
Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly
	195						200				205				
Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
	210						215				220				
Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys					
	225						230				235				

<210>	3	
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<212>	DNA	
<213>	Lama glama	
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<223>	n is a, c, g, or t	
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<223>	n is a, c, g, or t	
<220>		
<221>	modified_base	
<222>	(64)..(64)	
<223>	n is a, c, g, or t	
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	actnccagga ggccttctg tctttgtctt ccccccggaaa cccaggacg tcctctccat	120
	ttttggggc cgagtcacgt gcgttgtagt ggacgtcgga aagaaagacc cggaggtcaa	180
	tttcaactgg tatattgtatg gcgttgaggt gccaacggcc aatacgaagc caaaagagga	240
	acagttcaac agcacgtacc gcgtggtag cgtcctgccc atccagcacc aggactggct	300
	gacggggaaag gaattcaagt gcaaggtcaa caacaaagct ctccggcccc ccatcgagag	360
	gaccatctcc aaggccaaag ggcagacccg ggagccgcag gtgtacaccc tggccccaca	420
	ccggggaaagaa ctggccaaagg acaccgttag cgtaacatgc ctggtaaaag gtttctaccc	480
	agctgacatc aacgttgagt ggcagaggaa cggtcagccg gagtcagagg gcacctacgc	540

caacacgccc	ccacagctgg	acaacgacgg	gacctacttc	ctctacagca	agctctcggt	600
gggaaagaac	acgtggcagc	ggggagaaac	cttaacctgt	gtggtgatgc	atgaggccct	660
gcacaaccac	tacacccaga	aatccatcac	ccagtcttcg	ggtaaatagt	aatctaga	718

<210> 4

<211> 231

<212> PRT

<213> Lama glama

<400> 4

Glu	Pro	His	Gly	Gly	Cys	Thr	Cys	Pro	Gln	Cys	Pro	Ala	Pro	Glu	Leu
1															
														15	
Pro	Gly	Gly	Pro	Ser	Val	Phe	Val	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Val
														30	
Leu	Ser	Ile	Ser	Gly	Arg	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
														45	
Gly	Lys	Glu	Asp	Pro	Glu	Val	Asn	Phe	Asn	Trp	Tyr	Ile	Asp	Gly	Val
														60	
Glu	Val	Arg	Thr	Ala	Asn	Thr	Lys	Pro	Lys	Glu	Glu	Gln	Phe	Asn	Ser
														80	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Pro	Ile	Gln	His	Gln	Asp	Trp	Leu
														95	
Thr	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	Asn	Asn	Lys	Ala	Leu	Pro	Ala
														110	
Pro	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Thr	Arg	Glu	Pro
														125	
Gln	Val	Tyr	Thr	Leu	Ala	Pro	His	Arg	Glu	Glu	Leu	Ala	Lys	Asp	Thr
														140	
Val	Ser	Val	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ala	Asp	Ile	Asn
														160	
Val	Glu	Trp	Gln	Arg	Asn	Gly	Gln	Pro	Glu	Ser	Glu	Gly	Thr	Tyr	Ala
														175	
Asn	Thr	Pro	Pro	Gln	Leu	Asp	Asn	Asp	Gly	Thr	Tyr	Phe	Leu	Tyr	Ser
														190	
Arg	Leu	Ser	Val	Gly	Lys	Asn	Thr	Trp	Gln	Arg	Gly	Glu	Thr	Leu	Thr
														205	
Gly	Val	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser
														220	
Ile	Thr	Gln	Ser	Ser	Gly	Lys									
														230	

<210> 5

<211> 757

<212> DNA

<213> Lama glama

<400> 5

tgtatcaagaa	cccaagacac	caaaaccaca	accacaacca	caaccacaac	ccaatcctac	60
aacagaatcc	aagtgtccca	aatgtccagc	ccctgagctc	ctgggaggggc	cctcagtctt	120
catcttcccc	ccgaaaccca	aggacgtcct	ctccatttct	ggggaggccc	aggtcacgtg	180
cgttgtggta	gacgtgggccc	aggaagaccc	cgaggtcagt	ttcaactgggt	acattgtatgg	240
cgctgagggtg	cgaacggcca	acacgaggcc	aaaagaggaa	cagttcaaca	gcacgttaccc	300
cgtggtcagc	gtcctgcucca	tccagcacca	ggactggctg	acggggaaagg	aattcaagt	360
caaggtcaac	aacaaagctc	tcccggcccc	catcgagaag	accatctcca	aggccaaagg	420
gcagacccgg	gagccgcagg	tgtacaccct	ggccccacac	cgggaaagagc	tggccaagga	480
caccgtgagc	gtaacatgcc	tggtaaaagg	cttctaccca	cctgatatac	acgttgagt	540
gcagaggaat	gggcagccgg	agtcaagaggg	cacytacgcc	accacgcccac	cccagctgga	600
caacgacggg	acctacttcc	tctacagcaa	gctctcggtg	ggaaagaaca	cgtggcagca	660
gggagaaacc	ttcacctgtg	tggtgtatgc	cgaggccctg	cacaaccact	acacccagaa	720

atccatcacc cagtcccg gtaaatagta atctaga

757

<210> 6  
<211> 248  
<212> PRT  
<213> Lama glama  
<400> 6

Asp Gln Glu Pro Lys Thr Pro Lys Pro Gln Pro Gln Pro Gln  
1 5 10 15

Pro Asn Pro Thr Thr Glu Ser Lys Cys Pro Lys Cys Pro Ala Pro Glu  
20 25 30

Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp  
35 40 45

Val Leu Ser Ile Ser Gly Arg Pro Glu Val Thr Cys Val Val Val Asp  
50 55 60

Val Gly Gln Glu Asp Pro Glu Val Ser Phe Asn Trp Tyr Ile Asp Gly  
65 70 75 80

Ala Glu Val Arg Thr Ala Asn Thr Arg Pro Lys Glu Glu Gln Phe Asn  
85 90 95

Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln His Gln Asp Trp  
100 105 110

Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Ala Leu Pro  
115 120 125

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Thr Arg Glu  
130 135 140

Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu Leu Ala Lys Asp  
145 150 155 160

Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Tyr Pro Pro Asp Ile  
165 170 175

Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser Glu Gly Thr Tyr  
180 185 190

Ala Thr Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr Tyr Phe Leu Tyr  
195 200 205

Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln Gly Glu Thr Phe  
210 215 220

Thr Cys Val Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys  
225 230 235 240

Ser Ile Thr Gln Ser Ser Gly Lys  
245

<210> 7  
<211> 727  
<212> DNA  
<213> Lama glama  
<400> 7

tgatcaagcg caccacagcg aagaccccgag ctccaaagtgt cccaaatgcc caggccctga 60  
actccttggaa gggccacacgg tcttcatctt cccccccgaaa gccaaggacg tcctctccat 120  
cccccgaaaa cctgagggtca cgtgcttggc gtggacgtgg gtaaaagaaga ccctgagatc 180  
gagttcaagc tggccgtgg atgacacaga ggtacacacg gctgagacaa agccaaagga 240  
ggaacagttc aacagcacgt accgcgtggc cagcgtcctg cccatccagc accaggactg 300  
gctgacgggg aaggaatca agtgcacaggta caacaacaaa gctctccag ccccccattcga 360  
gaggaccatc tccaaaggcca aaggccacacg ccggggacccg caggtgtaca ccctggcccc 420  
acaccgggaa gagctggcca aggacaccgt gagegttaacc tgcctggta aaggcttctt 480  
cccagctgac atcaacgttg agtggcagag gaatggccag ccggagtcag agggcaccta 540  
cgccaaacacg ccggccacacg tggacaacga cgggacctac ttcctctaca gcaaactctc 600  
cgtggggaaag aacacgtggc agcagggaga agtcttcacc tgtgtggta tgcacgaggc 660  
tctacacaat cactccacccc agaaatccat caccctgtt ctcggtaaat agtaatctag 720

agggcc

727

<210> 8  
<211> 236  
<212> PRT  
<213> Lama glama  
<400> 8

Asp Gln Ala His His Ser Glu Asp Pro Ser Ser Lys Cys Pro Lys Cys  
1 5 10 15  
Pro Gly Pro Glu Leu Leu Gly Gly Pro Thr Val Phe Ile Phe Pro Pro  
20 25 30  
Lys Ala Lys Asp Val Leu Ser Ile Thr Arg Lys Pro Glu Val Thr Cys  
35 40 45  
Leu Trp Trp Thr Trp Val Lys Lys Thr Leu Arg Ser Ser Ser Trp  
50 55 60  
Ser Val Asp Asp Thr Glu Val His Thr Ala Glu Thr Lys Pro Lys Glu  
65 70 75 80  
Glu Gln Phe Asn Ser Thr Tyr Arg Val Val Ser Val Leu Pro Ile Gln  
85 90 95  
His Gln Asp Trp Leu Thr Gly Lys Glu Phe Lys Cys Lys Val Asn Asn  
100 105 110  
Lys Ala Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Ala Lys Gly  
115 120 125  
Gln Thr Arg Glu Pro Gln Val Tyr Thr Leu Ala Pro His Arg Glu Glu  
130 135 140  
Leu Ala Lys Asp Thr Val Ser Val Thr Cys Leu Val Lys Gly Phe Phe  
145 150 155 160  
Pro Ala Asp Ile Asn Val Glu Trp Gln Arg Asn Gly Gln Pro Glu Ser  
165 170 175  
Glu Gly Thr Tyr Ala Asn Thr Pro Pro Gln Leu Asp Asn Asp Gly Thr  
180 185 190  
Tyr Phe Leu Tyr Ser Lys Leu Ser Val Gly Lys Asn Thr Trp Gln Gln  
195 200 205  
Gly Glu Val Phe Thr Cys Val Val Met His Glu Ala Leu His Asn His  
210 215 220  
Ser Thr Gln Lys Ser Ile Thr Gln Ser Ser Gly Lys  
225 230 235

<210> 9  
<211> 54  
<212> DNA  
<213> Homo sapiens  
<400> 9

gatcaggagc ccaaatttt tgacaaaaact cacacatgcc caccgtgccc agca 54

<210> 10  
<211> 18  
<212> PRT  
<213> Homo sapiens  
<400> 10

Asp Gln Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
1 5 10 15  
Pro Ala

<210> 11  
<211> 54  
<212> DNA

<213> Homo sapiens  
<400> 11  
gatctggagc ccaaattctg tgacaaaact cacacatgcc caccgtgccc agca 54

<210> 12  
<211> 18  
<212> PRT  
<213> Homo sapiens  
<400> 12  
Asp Leu Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
1 5 10 15  
Pro Ala

<210> 13  
<211> 327  
<212> DNA  
<213> Homo sapiens  
<400> 13  
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atgatctccc ggacccctga ggtcacatgc gtggtggtgg acgtgagcca cgaagaccct 120  
gaggtcaagt tcaactggta cgtggacggc gtggaggtgc ataatgccaa gacaaagccg 180  
cgggaggagc agtacaacag cacgtaccgt gtggtcagcg tcctcaccgt cctgcaccag 240  
gactggctga atggcaagga gtacaagtgc aaggcttcca acaaagccct cccagccccc 300  
atcgagaaaa ccatctccaa agccaaa 327

<210> 14  
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<212> PRT  
<213> Homo sapiens  
<400> 14  
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro  
1 5 10 15  
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
20 25 30  
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val  
35 40 45  
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
50 55 60  
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln  
65 70 75 80  
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala  
85 90 95  
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys  
100 105

<210> 15  
<211> 324  
<212> DNA  
<213> Homo sapiens  
<400> 15  
gggcagccca gagaaccaca ggtgtacacc ctgccccat cccgggagga gatgaccaag 60  
aaccaggtaa gcctgacctg cctggtaaaa ggcttctatc ccagcgacat cgccgtggag 120  
tgggagagca atgggcagcc ggagaacaac tacaagacca cgcctccgt gctggactcc 180  
gacggctct tcttcctcta tagcaagctc accgtggaca agagcaggtg gcagcagggg 240  
aacgtttct catgctccgt gatgcatgag gctctgcaca accactacac gcagaagagc 300  
ctctccctgt ccccggttaa atga 324

<210> 16  
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Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly  
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